

#4

SEQUENCE LISTING

<110> KYOWA HAKKO KOGYO CO., LTD

<120> Novel Transaldolase

<130> 00005.001198

<140> US/10/088,594

<141> 2002-03-21

<150> JP 99/266548

<151> 1999-09-21

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<170> PatentIn Ver. 2.0

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<213> Corynebacterium glutamicum ATCC31388

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gac gac ctc tcc cgc gag cgc att act tcc ggc aat ctc agc cag gtt	96
Asp Asp Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val	
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Ile Glu Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe	
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gca gca gca atg tcc aag ggc gat tcc tac gac gct cag atc gca gag	192
Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu	
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Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser	
65 70 75 80	
atc gac gat gtt cgc aat gct tgt gat ctg ttc acc ggc atc ttc gag	288
Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu	
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Ile	Ser	Ala	Asp	Arg	Asp	Ala	Thr	Leu	Ala	Gln	Ala	Lys	Glu	Leu	Trp	
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ctg	cgc	ggc	aag	gca	ggc	gtt	gcc	aac	gct	cag	cgc	gct	tac	gct	gtg	720
Leu	Arg	Gly	Lys	Ala	Gly	Val	Ala	Asn	Ala	Gln	Arg	Ala	Tyr	Ala	Val	
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Tyr	Lys	Glu	Leu	Phe	Asp	Ala	Ala	Glu	Leu	Pro	Glu	Gly	Ala	Asn	Thr	
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290

295

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 Gln Leu Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu
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<212> DNA

<213> *Corynebacterium glutamicum* ATCC31388

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 Thr Val Arg Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala
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 Val Asp Thr Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly
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 Ser Gly His Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr
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Leu Tyr Gln Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala	
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Gly Arg Asp Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln	
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Tyr Ile Gln Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu	
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Arg His Thr Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly	
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Leu Phe Asp Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His	
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Glu Ala Ser Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val	
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Ala Glu Ala Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg	

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Trp	Gln	Val	Lys	Phe	Asp	Glu	Trp	Ala	Ala	Ala	Asn	Pro	Glu	Asn	Lys	
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Asp	Glu	Leu	Pro	Thr	Trp	Asp	Ala	Asp	Glu	Lys	Gly	Val	Ala	Thr	Arg	
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Lys	Ala	Ser	Glu	Ala	Ala	Leu	Gln	Ala	Leu	Gly	Lys	Thr	Leu	Pro	Glu	
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Ser	Ala	Glu	Pro	Tyr	Gly	Arg	Asn	Leu	His	Phe	Gly	Ile	Arg	Glu	His	
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Pro	Ala	Asp	Ala	Asn	Glu	Thr	Ala	Gln	Ala	Trp	Ala	Ala	Ala	Leu	Glu	
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Leu	Glu	Ala	Glu	Gly	Val	Ala	Ala	Arg	Val	Val	Ser	Val	Pro	Cys	Met	
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Asp	Trp	Phe	Gln	Glu	Gln	Asp	Ala	Glu	Tyr	Ile	Glu	Ser	Val	Leu	Pro	
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Ala	Ala	Val	Thr	Ala	Arg	Val	Ser	Val	Glu	Ala	Gly	Ile	Ala	Met	Pro	
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acc acc gat gca gtc gtg gca gcg gcc aag gac tcc att aac agt			2472
Thr Thr Asp Ala Val Val Ala Ala Ala Lys Asp Ser Ile Asn Ser			
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		Met Ser	
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cac att gat gat ctt gca cag ctc ggc act tcc act tgg ctc gac gac			2696
His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu Asp Asp			
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Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe Ala Ala			
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Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser Ile Asp			
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Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu Ser Ser			
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Leu	Pro	Ala	Ile	Thr	Asp	Ala	Leu	Ala	Glu	Gly	Ile	Ser	Val	Asn	Val		
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acc	ttg	atc	ttc	tcc	gtt	gct	cgc	tac	cgc	gag	gtc	atc	gct	gcg	tac	3176	
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Ile	Glu	Gly	Ile	Lys	Gln	Ala	Ala	Ala	Asn	Gly	His	Asp	Val	Ser	Lys		
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Ile	His	Ser	Val	Ala	Ser	Phe	Phe	Val	Ser	Arg	Val	Asp	Val	Glu	Ile		
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Asp	Lys	Arg	Leu	Glu	Ala	Ile	Gly	Ser	Asp	Glu	Ala	Leu	Ala	Leu	Arg		
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Gly	Lys	Ala	Gly	Val	Ala	Asn	Ala	Gln	Arg	Ala	Tyr	Ala	Val	Tyr	Lys		
			230					235					240				
gag	ctt	ttc	gac	gcc	gcc	gag	ctg	cct	gaa	ggt	gcc	aac	act	cag	cgc	3416	
Glu	Leu	Phe	Asp	Ala	Ala	Glu	Leu	Pro	Glu	Gly	Ala	Asn	Thr	Gln	Arg		
		245					250					255					
cca	ctg	tgg	gca	tcc	acc	ggc	gtg	aag	aac	cct	gcg	tac	gct	gca	act	3464	
Pro	Leu	Trp	Ala	Ser	Thr	Gly	Val	Lys	Asn	Pro	Ala	Tyr	Ala	Ala	Thr		
	260					265					270						
ctt	tac	gtt	tcc	gag	ctg	gct	ggt	cca	aac	acc	gtc	aac	acc	atg	cca	3512	
Leu	Tyr	Val	Ser	Glu	Leu	Ala	Gly	Pro	Asn	Thr	Val	Asn	Thr	Met	Pro		
275					280					285					290		
gaa	ggc	acc	atc	gac	gct	gtt	ctg	gaa	ctg	ggc	aac	ctg	cac	ggt	gac	3560	
Glu	Gly	Thr	Ile	Asp	Ala	Val	Leu	Glu	Leu	Gly	Asn	Leu	His	Gly	Asp		
				295					300					305			
acc	ctg	tcc	aac	tcc	gcg	gca	gaa	gct	gac	gct	gtg	ttc	tcc	cag	ctt	3608	
Thr	Leu	Ser	Asn	Ser	Ala	Ala	Glu	Ala	Asp	Ala	Val	Phe	Ser	Gln	Leu		
			310					315					320				
gag	gct	ctg	ggc	gtt	gac	ttg	gca	gat	gtc	ttc	cag	gtc	ctg	gag	acc	3656	
Glu	Ala	Leu	Gly	Val	Asp	Leu	Ala	Asp	Val	Phe	Gln	Val	Leu	Glu	Thr		
		325					330					335					

gag ggt gtg gac aag ttt gtt gct tct tgg agc gaa ctg ctt gag tcc 3704
Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu Glu Ser
340 345 350

atg gaa gct cgc ctg aag tagaatcagc acgctgcatc agtaacggcg 3752
Met Glu Ala Arg Leu Lys
355 360

acatgaaatc gaattagtgc gatcttatgt ggccggttaca catctttcat taaagaaagg 3812
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